

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/526,741
Source: PGT
Date Processed by STIC: 3-7-05

ENTERED



PCT

RAW SEQUENCE LISTING

DATE: 03/13/2005

PATENT APPLICATION: US/10/526,741

TIME: 12:03:02

Input Set : A:\PTO.FY.txt

Output Set: N:\CRF4\03132005\J526741.raw

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3 <110> APPLICANT: ABURATANI, Hiroyuki
4     MIDORIKAWA, Yutaka
5     NAKANO, Kiyotaka
6     OHIZUMI, Iwao
7     ITO, Yukio
8     TOKITA, Susumu
10 <120> TITLE OF INVENTION: ANTIBODY AGAINST SOLUBLE N-TERMINAL PEPTIDE OR C-TERMINAL
PEPTIDE OF GPC3
11     PRESENT IN BLOOD
W--> 0 <130> FILE REFERENCE:
C--> 13 <140> CURRENT APPLICATION NUMBER: US/10/526,741
C--> 14 <141> CURRENT FILING DATE: 2005-03-04
16 <150> PRIOR APPLICATION NUMBER: PCT/JP02/08999
17 <151> PRIOR FILING DATE: 2002-09-04
19 <160> NUMBER OF SEQ ID NOS: 24
21 <170> SOFTWARE: PatentIn Ver. 2.1
23 <210> SEQ ID NO: 1
24 <211> LENGTH: 31
25 <212> TYPE: DNA
26 <213> ORGANISM: Artificial Sequence
28 <220> FEATURE:
29 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
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35 <211> LENGTH: 31
36 <212> TYPE: DNA
37 <213> ORGANISM: Artificial Sequence
39 <220> FEATURE:
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45 <210> SEQ ID NO: 3
46 <211> LENGTH: 2300
47 <212> TYPE: DNA
48 <213> ORGANISM: Homo sapiens
50 <220> FEATURE:
51 <221> NAME/KEY: CDS
52 <222> LOCATION: (109)..(1851)
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56 gctccggctg ccactctccc gcgtctctct agctccctgc gaagcagg atg gcc ggg 117
57                                     Met Ala Gly
58                                     1

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59 acc gtg cgc acc gcg tgc ttg gtg gtg gcg atg ctg ctc agc ttg gac 165
60 Thr Val Arg Thr Ala Cys Leu Val Val Ala Met Leu Leu Ser Leu Asp
61      5      10      15
62 ttc ccg gga cag gcg cag ccc ccg ccg ccg ccg gac gcc acc tgt 213
63 Phe Pro Gly Gln Ala Gln Pro Pro Pro Pro Pro Pro Asp Ala Thr Cys
64 20      25      30      35
65 cac caa gtc cgc tcc ttc ttc cag aga ctg cag ccc gga ctc aag tgg 261
66 His Gln Val Arg Ser Phe Phe Gln Arg Leu Gln Pro Gly Leu Lys Trp
67      40      45      50
68 gtg cca gaa act ccc gtg cca gga tca gat ttg caa gta tgt ctc cct 309
69 Val Pro Glu Thr Pro Val Pro Gly Ser Asp Leu Gln Val Cys Leu Pro
70      55      60      65
71 aag ggc cca aca tgc tgc tca aga aag atg gaa gaa aaa tac caa cta 357
72 Lys Gly Pro Thr Cys Cys Ser Arg Lys Met Glu Glu Lys Tyr Gln Leu
73      70      75      80
74 aca gca cga ttg aac atg gaa cag ctg ctt cag tct gca agt atg gag 405
75 Thr Ala Arg Leu Asn Met Glu Gln Leu Leu Gln Ser Ala Ser Met Glu
76      85      90      95
77 ctc aag ttc tta att att cag aat gct gcg gtt ttc caa gag gcc ttt 453
78 Leu Lys Phe Leu Ile Ile Gln Asn Ala Ala Val Phe Gln Glu Ala Phe
79 100      105      110      115
80 gaa att gtt gtt cgc cat gcc aag aac tac acc aat gcc atg ttc aag 501
81 Glu Ile Val Val Arg His Ala Lys Asn Tyr Thr Asn Ala Met Phe Lys
82      120      125      130
83 aac aac tac cca agc ctg act cca caa gct ttt gag ttt gtg ggt gaa 549
84 Asn Asn Tyr Pro Ser Leu Thr Pro Gln Ala Phe Glu Phe Val Gly Glu
85      135      140      145
86 ttt ttc aca gat gtg tct ctc tac atc ttg ggt tct gac atc aat gta 597
87 Phe Phe Thr Asp Val Ser Leu Tyr Ile Leu Gly Ser Asp Ile Asn Val
88      150      155      160
89 gat gac atg gtc aat gaa ttg ttt gac agc ctg ttt cca gtc atc tat 645
90 Asp Asp Met Val Asn Glu Leu Phe Asp Ser Leu Phe Pro Val Ile Tyr
91      165      170      175
92 acc cag cta atg aac cca ggc ctg cct gat tca gcc ttg gac atc aat 693
93 Thr Gln Leu Met Asn Pro Gly Leu Pro Asp Ser Ala Leu Asp Ile Asn
94 180      185      190      195
95 gag tgc ctc cga gga gca aga cgt gac ctg aaa gta ttt ggg aat ttc 741
96 Glu Cys Leu Arg Gly Ala Arg Arg Asp Leu Lys Val Phe Gly Asn Phe
97      200      205      210
98 ccc aag ctt att atg acc cag gtt tcc aag tca ctg caa gtc act agg 789
99 Pro Lys Leu Ile Met Thr Gln Val Ser Lys Ser Leu Gln Val Thr Arg
100      215      220      225
101 atc ttc ctt cag gct ctg aat ctt gga att gaa gtg atc aac aca act 837
102 Ile Phe Leu Gln Ala Leu Asn Leu Gly Ile Glu Val Ile Asn Thr Thr
103      230      235      240
104 gat cac ctg aag ttc agt aag gac tgt ggc cga atg ctc acc aga atg 885
105 Asp His Leu Lys Phe Ser Lys Asp Cys Gly Arg Met Leu Thr Arg Met
106      245      250      255
107 tgg tac tgc tct tac tgc cag gga ctg atg atg gtt aaa ccc tgt ggc 933

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108	Trp	Tyr	Cys	Ser	Tyr	Cys	Gln	Gly	Leu	Met	Met	Val	Lys	Pro	Cys	Gly	
109	260					265					270					275	
110	ggt	tac	tgc	aat	gtg	gtc	atg	caa	ggc	tgt	atg	gca	ggt	gtg	gtg	gag	981
111	Gly	Tyr	Cys	Asn	Val	Val	Met	Gln	Gly	Cys	Met	Ala	Gly	Val	Val	Glu	
112					280					285						290	
113	att	gac	aag	tac	tgg	aga	gaa	tac	att	ctg	tcc	ctt	gaa	gaa	ctt	gtg	1029
114	Ile	Asp	Lys	Tyr	Trp	Arg	Glu	Tyr	Ile	Leu	Ser	Leu	Glu	Glu	Leu	Val	
115					295					300						305	
116	aat	ggc	atg	tac	aga	atc	tat	gac	atg	gag	aac	gta	ctg	ctt	ggt	ctc	1077
117	Asn	Gly	Met	Tyr	Arg	Ile	Tyr	Asp	Met	Glu	Asn	Val	Leu	Leu	Gly	Leu	
118					310					315						320	
119	ttt	tca	aca	atc	cat	gat	tct	atc	cag	tat	gtc	cag	aag	aat	gca	gga	1125
120	Phe	Ser	Thr	Ile	His	Asp	Ser	Ile	Gln	Tyr	Val	Gln	Lys	Asn	Ala	Gly	
121					325											335	
122	aag	ctg	acc	acc	act	att	ggc	aag	tta	tgt	gcc	cat	tct	caa	caa	cgc	1173
123	Lys	Leu	Thr	Thr	Thr	Ile	Gly	Lys	Leu	Cys	Ala	His	Ser	Gln	Gln	Arg	
124	340					345					350					355	
125	caa	tat	aga	tct	gct	tat	tat	cct	gaa	gat	ctc	ttt	att	gac	aag	aaa	1221
126	Gln	Tyr	Arg	Ser	Ala	Tyr	Tyr	Pro	Glu	Asp	Leu	Phe	Ile	Asp	Lys	Lys	
127					360					365						370	
128	gta	tta	aaa	gtt	gct	cat	gta	gaa	cat	gaa	gaa	acc	tta	tcc	agc	cga	1269
129	Val	Leu	Lys	Val	Ala	His	Val	Glu	His	Glu	Glu	Thr	Leu	Ser	Ser	Arg	
130					375					380						385	
131	aga	agg	gaa	cta	att	cag	aag	ttg	aag	tct	ttc	atc	agc	ttc	tat	agt	1317
132	Arg	Arg	Glu	Leu	Ile	Gln	Lys	Leu	Lys	Ser	Phe	Ile	Ser	Phe	Tyr	Ser	
133					390					395						400	
134	gct	ttg	cct	ggc	tac	atc	tgc	agc	cat	agc	cct	gtg	gcg	gaa	aac	gac	1365
135	Ala	Leu	Pro	Gly	Tyr	Ile	Cys	Ser	His	Ser	Pro	Val	Ala	Glu	Asn	Asp	
136					405					410						415	
137	acc	ctt	tgc	tgg	aat	gga	caa	gaa	ctc	gtg	gag	aga	tac	agc	caa	aag	1413
138	Thr	Leu	Cys	Trp	Asn	Gly	Gln	Glu	Leu	Val	Glu	Arg	Tyr	Ser	Gln	Lys	
139	420					425					430					435	
140	gca	gca	agg	aat	gga	atg	aaa	aac	cag	ttc	aat	ctc	cat	gag	ctg	aaa	1461
141	Ala	Ala	Arg	Asn	Gly	Met	Lys	Asn	Gln	Phe	Asn	Leu	His	Glu	Leu	Lys	
142					440						445					450	
143	atg	aag	ggc	cct	gag	cca	gtg	gtc	agt	caa	att	att	gac	aaa	ctg	aag	1509
144	Met	Lys	Gly	Pro	Glu	Pro	Val	Val	Ser	Gln	Ile	Ile	Asp	Lys	Leu	Lys	
145					455					460						465	
146	cac	att	aac	cag	ctc	ctg	aga	acc	atg	tct	atg	ccc	aaa	ggt	aga	gtt	1557
147	His	Ile	Asn	Gln	Leu	Leu	Arg	Thr	Met	Ser	Met	Pro	Lys	Gly	Arg	Val	
148					470					475						480	
149	ctg	gat	aaa	aac	ctg	gat	gag	gaa	ggg	ttt	gaa	agt	gga	gac	tgc	ggt	1605
150	Leu	Asp	Lys	Asn	Leu	Asp	Glu	Glu	Gly	Phe	Glu	Ser	Gly	Asp	Cys	Gly	
151					485					490						495	
152	gat	gat	gaa	gat	gag	tgc	att	gga	ggc	tct	ggt	gat	gga	atg	ata	aaa	1653
153	Asp	Asp	Glu	Asp	Glu	Cys	Ile	Gly	Gly	Ser	Gly	Asp	Gly	Met	Ile	Lys	
154	500					505					510					515	
155	gtg	aag	aat	cag	ctc	cgc	ttc	ctt	gca	gaa	ctg	gcc	tat	gat	ctg	gat	1701
156	Val	Lys	Asn	Gln	Leu	Arg	Phe	Leu	Ala	Glu	Leu	Ala	Tyr	Asp	Leu	Asp	

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157          520          525          530
158 gtg gat gat gcg cct gga aac agt cag cag gca act ccg aag gac aac 1749
159 Val Asp Asp Ala Pro Gly Asn Ser Gln Gln Ala Thr Pro Lys Asp Asn
160          535          540          545
161 gag ata agc acc ttt cac aac ctc ggg aac gtt cat tcc ccg ctg aag 1797
162 Glu Ile Ser Thr Phe His Asn Leu Gly Asn Val His Ser Pro Leu Lys
163          550          555          560
164 ctt ctc acc agc atg gcc atc tcg gtg gtg tgc ttc ttc ttc ctg gtg 1845
165 Leu Leu Thr Ser Met Ala Ile Ser Val Val Cys Phe Phe Phe Leu Val
166          565          570          575
167 cac tga ctgcctggtg cccagcacat gtgctgccct acagcaccct gtggtcttcc 1901
168 His
169 580
170 tcgataaagg gaaccacttt cttatTTTTT tctatTTTTT tttttttggt atcctgtata 1961
171 cctcctccag ccatgaagta gaggactaac catgtgttat gttttcgaaa atcaaaggt 2021
172 atcttttggg ggaagataca ttttagtggt agcatataga ttgtcctttt gcaaagaaag 2081
173 aaaaaaaacc atcaagttgt gccaaattat tctcctatgt ttggctgcta gaacatggtt 2141
174 accatgtctt tctctctcac tccctccctt tctatcgttc tctctttgca tggatttctt 2201
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180 <212> TYPE: PRT
181 <213> ORGANISM: Homo sapiens
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188 Ala Thr Cys His Gln Val Arg Ser Phe Phe Gln Arg Leu Gln Pro Gly
189 35 40 45
190 Leu Lys Trp Val Pro Glu Thr Pro Val Pro Gly Ser Asp Leu Gln Val
191 50 55 60
192 Cys Leu Pro Lys Gly Pro Thr Cys Cys Ser Arg Lys Met Glu Glu Lys
193 65 70 75 80
194 Tyr Gln Leu Thr Ala Arg Leu Asn Met Glu Gln Leu Leu Gln Ser Ala
195 85 90 95
196 Ser Met Glu Leu Lys Phe Leu Ile Ile Gln Asn Ala Ala Val Phe Gln
197 100 105 110
198 Glu Ala Phe Glu Ile Val Val Arg His Ala Lys Asn Tyr Thr Asn Ala
199 115 120 125
200 Met Phe Lys Asn Asn Tyr Pro Ser Leu Thr Pro Gln Ala Phe Glu Phe
201 130 135 140
202 Val Gly Glu Phe Phe Thr Asp Val Ser Leu Tyr Ile Leu Gly Ser Asp
203 145 150 155 160
204 Ile Asn Val Asp Asp Met Val Asn Glu Leu Phe Asp Ser Leu Phe Pro
205 165 170 175
206 Val Ile Tyr Thr Gln Leu Met Asn Pro Gly Leu Pro Asp Ser Ala Leu
207 180 185 190

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208 Asp Ile Asn Glu Cys Leu Arg Gly Ala Arg Arg Asp Leu Lys Val Phe
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210 Gly Asn Phe Pro Lys Leu Ile Met Thr Gln Val Ser Lys Ser Leu Gln
211      210          215          220
212 Val Thr Arg Ile Phe Leu Gln Ala Leu Asn Leu Gly Ile Glu Val Ile
213 225          230          235          240
214 Asn Thr Thr Asp His Leu Lys Phe Ser Lys Asp Cys Gly Arg Met Leu
215          245          250          255
216 Thr Arg Met Trp Tyr Cys Ser Tyr Cys Gln Gly Leu Met Met Val Lys
217          260          265          270
218 Pro Cys Gly Gly Tyr Cys Asn Val Val Met Gln Gly Cys Met Ala Gly
219          275          280          285
220 Val Val Glu Ile Asp Lys Tyr Trp Arg Glu Tyr Ile Leu Ser Leu Glu
221      290          295          300
222 Glu Leu Val Asn Gly Met Tyr Arg Ile Tyr Asp Met Glu Asn Val Leu
223 305          310          315          320
224 Leu Gly Leu Phe Ser Thr Ile His Asp Ser Ile Gln Tyr Val Gln Lys
225          325          330          335
226 Asn Ala Gly Lys Leu Thr Thr Thr Ile Gly Lys Leu Cys Ala His Ser
227          340          345          350
228 Gln Gln Arg Gln Tyr Arg Ser Ala Tyr Tyr Pro Glu Asp Leu Phe Ile
229          355          360          365
230 Asp Lys Lys Val Leu Lys Val Ala His Val Glu His Glu Glu Thr Leu
231      370          375          380
232 Ser Ser Arg Arg Arg Glu Leu Ile Gln Lys Leu Lys Ser Phe Ile Ser
233 385          390          395          400
234 Phe Tyr Ser Ala Leu Pro Gly Tyr Ile Cys Ser His Ser Pro Val Ala
235          405          410          415
236 Glu Asn Asp Thr Leu Cys Trp Asn Gly Gln Glu Leu Val Glu Arg Tyr
237          420          425          430
238 Ser Gln Lys Ala Ala Arg Asn Gly Met Lys Asn Gln Phe Asn Leu His
239          435          440          445
240 Glu Leu Lys Met Lys Gly Pro Glu Pro Val Val Ser Gln Ile Ile Asp
241      450          455          460
242 Lys Leu Lys His Ile Asn Gln Leu Leu Arg Thr Met Ser Met Pro Lys
243 465          470          475          480
244 Gly Arg Val Leu Asp Lys Asn Leu Asp Glu Glu Gly Phe Glu Ser Gly
245          485          490          495
246 Asp Cys Gly Asp Asp Glu Asp Glu Cys Ile Gly Gly Ser Gly Asp Gly
247          500          505          510
248 Met Ile Lys Val Lys Asn Gln Leu Arg Phe Leu Ala Glu Leu Ala Tyr
249          515          520          525
250 Asp Leu Asp Val Asp Asp Ala Pro Gly Asn Ser Gln Gln Ala Thr Pro
251      530          535          540
252 Lys Asp Asn Glu Ile Ser Thr Phe His Asn Leu Gly Asn Val His Ser
253 545          550          555          560
254 Pro Leu Lys Leu Leu Thr Ser Met Ala Ile Ser Val Val Cys Phe Phe
255          565          570          575
256 Phe Leu Val His

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RAW SEQUENCE LISTING ERROR SUMMARY
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Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 10

VERIFICATION SUMMARY

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Input Set : A:\PTO.FY.txt

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L:0 M:201 W: Mandatory field data missing, <130> FILE REFERENCE
L:13 M:270 C: Current Application Number differs, Replaced Current Application Number
L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:410 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:10
L:583 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:12
L:758 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:14
L:933 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:16
L:1063 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:18
L:1163 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:20
L:1263 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:22
L:1363 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:24